

RAW SEQUENCE LISTING

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Application Serial Number: 10/693, 4804
Source: JFW/6
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PATENT APPLICATION: US/10/693,480A

DATE: 08/03/2006

TIME: 08:59:01

Input Set : A:\66602-B.txt
 Output Set: N:\CRF4\08032006\J693480A.raw

3 <110> APPLICANT: ITESCU, SILVIU
 5 <120> TITLE OF INVENTION: REGENERATION OF ENDOGENOUS MYOCARDIAL TISSUE
 7 <130> FILE REFERENCE: 0575/66602B
 9 <140> CURRENT APPLICATION NUMBER: 10/693,480A
 10 <141> CURRENT FILING DATE: 2003-10-23
 12 <150> PRIOR APPLICATION NUMBER: 10/128,738
 13 <151> PRIOR FILING DATE: 2002-04-23
 15 <160> NUMBER OF SEQ ID NOS: 11
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2780
 21 <212> TYPE: DNA
 22 <213> ORGANISM: HOMO SAPIENS
 24 <400> SEQUENCE: 1
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 29 ttaggcgcct ttcgaaaac ctatgtatata atattcattt gtttaatct tattttat 180
 31 ttaagctcaa actgcttaag aataccttaa ttccctaaag tgaaataatt ttttgcaaag 240
 33 gggtttcctc gatttggagc ttttttttc ttccaccgtc atttctaact cttaaaacca 300
 35 actcagttcc atcatggta tggcaagaa gatcaagtct ttgaggtgg tcttaacga 360
 37 ccctgaaaag gtgtacggca gtggcgagaa ggtggctggc cgggtgatag tggaggtgtg 420
 39 tgaagttact cggtcaaaag ccgttaggt cctggctgc ggagtggcta aagtctttg 480
 41 gatgcaggga tcccagcgt gcaaacaacac ttcggagtagt ctgcgtatg aagacacgct 540
 43 tctctggaa gaccagccaa caggtgagaa tgagatggtg atcatgagac ctggaaacaa 600
 45 atatgagttac aagttcggtc tttagcttc tcaggccct ctggaaacat ctttcaaagg 660
 47 aaaatatggg tggtagact actgggtgaa ggctttctt gaccggccga gccagccaac 720
 49 tcaagagaca aagaaaaact tggaaatgtt ggtatggtg gatgtcaata cccctgattt 780
 51 aatggcacct gtgtctgcta aaaaagaaaa gaaagttcc tgcgttca ttccctgatgg 840
 53 gcgggtgtct gtctctgctc gaattgacag aaaaggattc tgtgaagggtg atgagatttc 900
 55 catccatgtc gactttgaga atacatgttc ccgaattgtg gtccccaaag ctgcattgt 960
 57 ggccgcac acttacctt ccaatggcca gaccaagggtg ctgactcaga agttgtcatc 1020
 59 agtcagggc aatcatatta ttcaggggac atgcgtatca tggcgatggc agagccctcg 1080
 61 gttcagaag atcaggccctt ctatcctggg ctgcacatc ctgcgtatg aatattcctt 1140
 63 actgatctat gttagcttc ctggatccaa gaaggatcgtt ctgcgtatc ccctggtaat 1200
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 69 tgtcattcct gaagatcacc gattggagag cccaaaccact cctctgtatg atgacatgg 1380
 71 tggctctcaa gacagccata tctttatgtt tgccctgtatc tcaagttca tgccaccacc 1440
 73 gacttatact gaggtggatc cttgcatttca caacaacaat gtgcgtatg catgtggaa 1500
 75 aaaaagaagca gctttaccta ctgtttctt ttgtctctc ttcctggaca ctcactttt 1560
 77 cagagactca acagtctcg caatggatgt tgggtccacc ttagcctctg acttccataat 1620
 79 gtaggaggtg gtcagcaggc aatctcctgg gccttaaagg atgcggactc atcctcagcc 1680
 81 agcgcccatg ttgtataca ggggtgtttt ttggatgggt taaaaataaa cttagaaaaac 1740

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83	tcaggcccattc	ccatTTTCTC	agatCTCCTT	gaaaATTGAG	gcCTTTCGA	tagTTTGGG	1800									
85	tcaGGtaaaa	atggCCtCCT	ggCGtaAGCT	tttcaAGGTT	ttttGGAGGC	tttttGtaaa	1860									
87	ttgtgatagg	aactTTGGAC	cttgaACTTA	cgtatCATGT	ggagaAGAGC	caatttaACA	1920									
89	aacttaggaag	atgaaaAGGG	aaattgtGGC	caaaACTTTG	ggaaaAGGAG	gttCTTaaa	1980									
91	tcaGtgtttc	ccCTTGTGc	acttGtagaa	aaaaaAGAAA	aacTTCTAG	agctGATTTG	2040									
93	atggacaatg	gagagAGCTT	tccCTGTGAT	tataaaaaAG	gaagCTAGT	gctCTACGGT	2100									
95	cacTttGCT	taagAGATA	cttaACCTG	gctttAAAG	cagtGTAAC	tgccccACCA	2160									
97	aaggCttAA	aaggCATTtT	tggAGCCTAT	tgcactGTGT	tctCCTACTG	caaataTTT	2220									
99	catatGGGAG	gatGGTTTTC	tcttCATGTA	agtCCttGGA	attGATTCTA	aggTGATGTT	2280									
101	cttagCactt	taattCCTGT	caaattttt	gttCTCCCt	tctGCCATCT	taaatGTAAG	2340									
103	ctgaaaACTGG	tctactGTGT	ctctAGGTT	aagCCAAAAG	acaaaaaaaaa	tttactact	2400									
105	tttGAGATTG	ccccAAgtTA	cagaATTATA	taattCTAAC	gcttaAAATCA	tgtGAAAGGG	2460									
107	ttGCTGCTGT	cAGCCTGcc	cactGTGACT	tcaAAACCCAA	ggagGAACtC	ttGATCAAGA	2520									
109	tGCCCAACCC	tgtGATCAGA	acctCCAAAT	actGCCATGA	gaaACTAGAG	ggcAGGTCTT	2580									
111	cataAAAGCC	cttGAAACCC	cTTCCtGcc	ctgtGTTAGG	agatAGGGAT	attGGCCCT	2640									
113	cactGcAGCT	gccAGCATT	ggtcAGTcac	tctcAGCCAT	agcactTTGT	tcaCTGTCCT	2700									
115	gtGTCAGAGC	actGAGCTCC	accCTTTCT	gagAGTTATT	acAGCCAGAA	agtGTGGGCT	2760									
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128	1				5				10					15		
131	Pro	Glu	Lys	Val	Tyr	Gly	Ser	Gly	Glu	Lys	Val	Ala	Gly	Arg	Val	Ile
132					20				25					30		
135	Val	Glu	Val	Cys	Glu	Val	Thr	Arg	Val	Lys	Ala	Val	Arg	Ile	Leu	Ala
136					35				40					45		
139	Cys	Gly	Val	Ala	Lys	Val	Leu	Trp	Met	Gln	Gly	Ser	Gln	Gln	Cys	Lys
140					50				55					60		
143	Gln	Thr	Ser	Glu	Tyr	Leu	Arg	Tyr	Glu	Asp	Thr	Leu	Leu	Glu	Asp	
144	65				65				70					75		80
147	Gln	Pro	Thr	Gly	Glu	Asn	Glu	Met	Val	Ile	Met	Arg	Pro	Gly	Asn	Lys
148					85				90					95		
151	Tyr	Glu	Tyr	Lys	Phe	Gly	Phe	Glu	Leu	Pro	Gln	Gly	Pro	Leu	Gly	Thr
152					100				105					110		
155	Ser	Phe	Lys	Gly	Lys	Tyr	Gly	Val	Asp	Tyr	Trp	Val	Lys	Ala	Phe	
156					115				120					125		
159	Leu	Asp	Arg	Pro	Ser	Gln	Pro	Thr	Gln	Glu	Thr	Lys	Lys	Asn	Phe	Glu
160					130				135					140		
163	Val	Val	Asp	Leu	Val	Asp	Val	Asn	Thr	Pro	Asp	Leu	Met	Ala	Pro	Val
164	145				145				150					155		160
167	Ser	Ala	Lys	Lys	Glu	Lys	Lys	Val	Ser	Cys	Met	Phe	Ile	Pro	Asp	Gly
168					165				165					170		175
171	Arg	Val	Ser	Val	Ser	Ala	Arg	Ile	Asp	Arg	Lys	Gly	Phe	Cys	Glu	Gly
172					180				185					185		190
175	Asp	Glu	Ile	Ser	Ile	His	Ala	Asp	Phe	Glu	Asn	Thr	Cys	Ser	Arg	Ile
176					195				200					205		

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180	210						215					220				
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184	225						230				235			240		
187	His	Ile	Ile	Ser	Gly	Thr	Cys	Ala	Ser	Trp	Arg	Gly	Lys	Ser	Leu	Arg
188							245			250			255			
191	Val	Gln	Lys	Ile	Arg	Pro	Ser	Ile	Leu	Gly	Cys	Asn	Ile	Leu	Arg	Val
192							260			265			270			
195	Glu	Tyr	Ser	Leu	Leu	Ile	Tyr	Val	Ser	Val	Pro	Gly	Ser	Lys	Lys	Val
196							275			280			285			
199	Ile	Leu	Asp	Leu	Pro	Leu	Val	Ile	Gly	Ser	Arg	Ser	Gly	Leu	Ser	Ser
200							290			295			300			
203	Arg	Thr	Ser	Ser	Met	Ala	Ser	Arg	Thr	Ser	Ser	Glu	Met	Ser	Trp	Val
204	305						310				315			320		
207	Asp	Leu	Asn	Ile	Pro	Asp	Thr	Pro	Glu	Ala	Pro	Pro	Cys	Tyr	Met	Asp
208							325			330			335			
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212							340			345			350			
215	Asp	Asp	Met	Asp	Gly	Ser	Gln	Asp	Ser	Pro	Ile	Phe	Met	Tyr	Ala	Pro
216							355			360			365			
219	Glu	Phe	Lys	Phe	Met	Pro	Pro	Pro	Thr	Tyr	Thr	Glu	Val	Asp	Pro	Cys
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237	gtcaaaagccg	ttaggatcct	ggcttgcgga	gtggctaaag	tgcttgcgat	gcagggtatcc								180		
239	cagcagtgc	aacagacttc	ggagtagcctg	cgctatgaag	acacgcttct	tctggaaagac								240		
241	cagccaaacag	gtgagaatga	gatggtgatc	atgagacctg	gaaacaaata	tgagttacaag								300		
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253	tttgagaata	catgtcccc	aatttgtggc	cccaaagctg	ccattgtggc	ccgccacact								660		
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259	aggccttcta	tcctggctg	caacatcctt	cgagttgaat	attccttact	gatctatgtt								840		
261	agcgccctgt	gatccaagaa	ggtcatcctt	gacctgcccc	tggtaattgg	cagcagatca								900		
263	ggtctaagca	gcagaacatc	cacatggccc	agccgaacca	gctctgagat	gagttgggt								960		
265	gatctgaaca	tccctgtatc	cccagaagct	cctccctgt	atatggatgt	cattcctgaa								1020		
267	gatcaccgat	tggagagccc	aaccactcct	ctgtctatgt	acatggatgg	ctctcaagac								1080		
269	agcccttatct	ttatgtatgc	ccctgagttc	aagtcatgc	caccaccgac	ttatactgag								1140		
271	gtggatccct	gcatcctcaa	caacaatgtg	cagtga										1176		

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274 <210> SEQ ID NO: 4
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 280 <223> OTHER INFORMATION: PRIMER DIRETCTED TO RAT Cinc
 282 <400> SEQUENCE: 4 20
 283 gaagatagat tgcaccgatg
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 287 <211> LENGTH: 18
 288 <212> TYPE: DNA
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 298 <210> SEQ ID NO: 6
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 318 <400> SEQUENCE: 7 28
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 322 <210> SEQ ID NO: 8
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 324 <212> TYPE: DNA
 325 <213> ORGANISM: ARTIFICIAL SEQUENCE
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 339 <220> FEATURE:
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 346 <210> SEQ ID NO: 10

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358 <210> SEQ ID NO: 11
359 <211> LENGTH: 23
360 <212> TYPE: DNA
361 <213> ORGANISM: ARTIFICIAL SEQUENCE
363 <220> FEATURE:
364 <223> OTHER INFORMATION: PRIMER DIRECTED TO RAT HBP23
366 <400> SEQUENCE: 11
367 ccagctgggc acacttcacc atg 23

VERIFICATION SUMMARY

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